

SEQUENCE LISTING

<110> Kramer, Michael

<120> Regulatory Protein pKe#83 from Human
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<130> km-3/PCT

<140> PCT/DE99/03732

<141> 1999-11-19

<150> DE19854672.6

<151> 1998-11-26

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<151> 1998-12-07

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<170> PatentIn Ver. 2.1

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<223> Phosphorylation sites: 9x Protein kinase, 15x
Caseine kinase, 2x Tyrosine kinase

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Arg Ser Leu Glu Cys Arg Ser Asp Pro Glu Ser Pro Ile Lys Lys Thr
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Ser Leu Ser Pro Thr Ser Lys Leu Gly Tyr Ser Tyr Ser Arg Asp Leu
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Asp Leu Ala Lys Lys Lys His Ala Ser Leu Arg Gln Thr Glu Ser Asp
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Pro Asp Ala Asp Arg Thr Thr Leu Asn His Ala Asp His Ser Ser Lys
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Ile Val Gln His Arg Leu Leu Ser Arg Gln Glu Glu Leu Lys Glu Arg
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```

```

<210> 6
<211> 487
<212> PRT
<213> Homo sapiens

```

```

<220>
<223> Phosphorylation sites: 8x Protein kinase,12x
      Caseine kinase, 2x Tyrosine kinase

```

```

<220>
<223> Prenylation site (CAAX-box)

```

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      20             25             30

Arg Ser Leu Glu Cys Arg Ser Asp Pro Glu Ser Pro Ile Lys Lys Thr
      35             40             45

Ser Leu Ser Pro Thr Ser Lys Leu Gly Tyr Ser Tyr Ser Arg Asp Leu
      50             55             60

Asp Leu Ala Lys Lys Lys His Ala Ser Leu Arg Gln Thr Glu Ser Asp
      65             70             75             80

Pro Asp Ala Asp Arg Thr Thr Leu Asn His Ala Asp His Ser Ser Lys
      85             90             95

Ile Val Gln His Arg Leu Leu Ser Arg Gln Glu Glu Leu Lys Glu Arg
      100            105            110

```

Ala	Arg	Val	Leu	Leu	Glu	Gln	Ala	Arg	Arg	Asp	Ala	Ala	Leu	Lys	Ala		
		115					120					125					
Gly	Asn	Lys	His	Asn	Thr	Asn	Thr	Ala	Thr	Pro	Phe	Cys	Asn	Arg	Gln		
	130					135					140						
Leu	Ser	Asp	Gln	Gln	Asp	Glu	Glu	Arg	Arg	Arg	Gln	Leu	Arg	Glu	Arg		
145					150					155					160		
Ala	Arg	Gln	Leu	Ile	Ala	Glu	Ala	Arg	Ser	Gly	Val	Lys	Met	Ser	Glu		
				165					170					175			
Leu	Pro	Ser	Tyr	Gly	Glu	Met	Ala	Ala	Glu	Lys	Leu	Lys	Glu	Arg	Ser		
			180					185					190				
Lys	Ala	Ser	Gly	Glu	Gln	Asn	Ser	Lys	Leu	Val	Asp	Leu	Lys	Leu	Lys		
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Lys	Leu	Leu	Glu	Val	Gln	Pro	Gln	Val	Ala	Asn	Ser	Pro	Ser	Ser	Ala		
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Ala	Gln	Lys	Ala	Val	Thr	Glu	Ser	Ser	Glu	Gln	Asp	Met	Lys	Ser	Gly		
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Thr	Glu	Asp	Leu	Arg	Thr	Glu	Arg	Leu	Gln	Lys	Thr	Thr	Glu	Arg	Phe		
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Arg	Asn	Pro	Val	Val	Phe	Ser	Lys	Asp	Ser	Thr	Val	Arg	Lys	Thr	Gln		
			260					265					270				
Leu	Gln	Ser	Phe	Ser	Gln	Tyr	Ile	Glu	Asn	Arg	Pro	Glu	Met	Lys	Arg		
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Gln	Arg	Ser	Ile	Gln	Glu	Asp	Thr	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Ala		
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Ala	Ile	Thr	Glu	Thr	Gln	Arg	Lys	Pro	Ser	Glu	Asp	Glu	Val	Leu	Asn		
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				325					330					335			
Leu	Glu	Asn	Glu	Gln	Lys	Gln	Ile	Asp	Thr	Arg	Ala	Ala	Leu	Val	Glu		
			340					345					350				
Lys	Arg	Leu	Arg	Tyr	Leu	Met	Asp	Thr	Gly	Arg	Asn	Thr	Glu	Glu	Glu		
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Glu	Ala	Met	Met	Gln	Glu	Trp	Phe	Met	Leu	Val	Asn	Lys	Lys	Asn	Ala		

370	375	380
Leu Ile Arg Arg Met Asn Gln Leu Ser Leu Leu Glu Lys Glu His Asp 385 390 395 400		
Leu Glu Arg Arg Tyr Glu Leu Leu Asn Arg Glu Leu Arg Ala Met Leu 405 410 415		
Ala Ile Glu Asp Trp Gln Lys Thr Glu Ala Gln Lys Arg Arg Glu Gln 420 425 430		
Leu Leu Leu Asp Glu Leu Val Ala Leu Val Asn Lys Arg Asp Ala Leu 435 440 445		
Val Arg Asp Leu Asp Ala Gln Glu Lys Gln Ala Glu Glu Glu Asp Glu 450 455 460		
His Leu Glu Arg Thr Leu Glu Gln Asn Lys Gly Lys Met Ala Lys Lys 465 470 475 480		
Glu Glu Lys Cys Val Leu Gln 485		

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 <211> 4914
 <212> DNA
 <213> Homo sapiens

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 80
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```

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040

```

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```

```

<210> 8
<211> 1076
<212> PRT
<213> Homo sapiens

<220>
<223> Phosphorylation sites: 24x Protein kinase, 29x
      Caseine kinase, 5x Tyrosine kinase

<220>
<223> 8 Myristillation sites

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  1              5              10              15

Lys  Phe  Lys  Pro  Leu  Ser  Lys  Lys  Val  Val  Ser  Ala  Ala  Leu  Gln  Phe
              20              25              30

Ser  Leu  Ser  Cys  Ile  Phe  Leu  Arg  Glu  Gly  Lys  Ala  Thr  Asp  Glu  Asp
          35              40              45

Met  Gln  Ser  Leu  Ala  Ser  Leu  Val  Ser  Met  Lys  Gln  Ala  Asp  Ile  Gly
  50              55              60

Asn  Leu  Asp  Asp  Phe  Glu  Glu  Asp  Asn  Glu  Asp  Asp  Asp  Glu  Asn  Arg
  65              70              75              80

Val  Asn  Gln  Glu  Glu  Lys  Ala  Ala  Lys  Ile  Thr  Glu  Leu  Ile  Asn  Lys
          85              90              95

Leu  Asn  Phe  Leu  Asp  Glu  Ala  Glu  Lys  Asp  Leu  Ala  Thr  Val  Asn  Ser
          100             105             110

Asn  Pro  Phe  Asp  Asp  Pro  Asp  Ala  Ala  Glu  Leu  Asn  Pro  Phe  Gly  Asp
          115             120             125

Pro  Asp  Ser  Glu  Glu  Pro  Ile  Thr  Glu  Thr  Ala  Ser  Pro  Arg  Lys  Thr
          130             135             140

Glu  Asp  Ser  Phe  Tyr  Asn  Asn  Ser  Tyr  Asn  Pro  Phe  Lys  Glu  Val  Gln
  145             150             155             160

```

Thr	Pro	Gln	Tyr	Leu	Asn	Pro	Phe	Asp	Glu	Pro	Glu	Ala	Phe	Val	Thr	
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			180					185					190			
Val	Asp	Met	Ser	Lys	Tyr	Leu	Tyr	Ala	Asp	Ser	Ser	Lys	Thr	Glu	Glu	
		195					200					205				
Glu	Glu	Leu	Asp	Glu	Ser	Asn	Pro	Phe	Tyr	Glu	Pro	Lys	Ser	Thr	Pro	
	210					215					220					
Pro	Pro	Asn	Asn	Leu	Val	Asn	Pro	Val	Gln	Glu	Leu	Glu	Thr	Glu	Arg	
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Arg	Val	Lys	Arg	Lys	Ala	Pro	Ala	Pro	Pro	Val	Leu	Ser	Pro	Lys	Thr	
				245					250					255		
Gly	Val	Leu	Asn	Glu	Asn	Thr	Val	Ser	Ala	Gly	Lys	Asp	Leu	Ser	Thr	
			260					265					270			
Ser	Pro	Lys	Pro	Ser	Pro	Ile	Pro	Ser	Pro	Val	Leu	Gly	Arg	Lys	Pro	
		275					280					285				
Asn	Ala	Ser	Gln	Ser	Leu	Leu	Val	Trp	Cys	Lys	Glu	Val	Thr	Lys	Asn	
	290					295					300					
Tyr	Arg	Gly	Val	Lys	Ile	Thr	Asn	Phe	Thr	Thr	Ser	Trp	Arg	Asn	Gly	
305					310					315					320	
Leu	Ser	Phe	Cys	Ala	Ile	Leu	His	His	Phe	Arg	Pro	Asp	Leu	Ile	Asp	
				325					330					335		
Tyr	Lys	Ser	Leu	Asn	Pro	Gln	Asp	Ile	Lys	Glu	Asn	Asn	Lys	Lys	Ala	
			340					345					350			
Tyr	Asp	Gly	Phe	Ala	Ser	Ile	Gly	Ile	Ser	Arg	Leu	Leu	Glu	Pro	Ser	
		355					360					365				
Asp	Met	Val	Leu	Leu	Ala	Ile	Pro	Asp	Lys	Leu	Thr	Val	Met	Thr	Tyr	
	370					375					380					
Leu	Tyr	Gln	Ile	Arg	Ala	His	Phe	Ser	Gly	Gln	Glu	Leu	Asn	Val	Val	
385					390					395					400	
Gln	Ile	Glu	Glu	Asn	Ser	Ser	Lys	Ser	Thr	Tyr	Lys	Val	Gly	Asn	Tyr	
				405					410					415		

Glu	Thr	Asp	Thr	Asn	Ser	Ser	Val	Asp	Gln	Glu	Lys	Phe	Tyr	Ala	Glu	
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Leu	Ser	Asp	Leu	Lys	Arg	Glu	Pro	Glu	Leu	Gln	Gln	Pro	Ile	Ser	Gly	
		435					440					445				
Ala	Val	Asp	Phe	Leu	Ser	Gln	Asp	Asp	Ser	Val	Phe	Val	Asn	Asp	Ser	
	450					455					460					
Gly	Val	Gly	Glu	Ser	Glu	Ser	Glu	His	Gln	Thr	Pro	Asp	Asp	His	Leu	
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				485					490					495		
Glu	Pro	Gln	Lys	Ser	Gln	Gln	Ser	Ser	Gly	Arg	Thr	Ser	Gly	Ser	Asp	
			500					505					510			
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		515					520					525				
Leu	Gly	Lys	Lys	Arg	Leu	Leu	Lys	Ala	Glu	Thr	Leu	Glu	Leu	Ser	Asp	
	530					535					540					
Leu	Tyr	Val	Ser	Asp	Lys	Lys	Lys	Asp	Met	Ser	Pro	Pro	Phe	Ile	Cys	
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Glu	Glu	Thr	Asp	Glu	Gln	Lys	Leu	Gln	Thr	Leu	Asp	Ile	Gly	Ser	Asn	
				565					570					575		
Leu	Glu	Lys	Glu	Lys	Leu	Glu	Asn	Ser	Arg	Ser	Leu	Glu	Cys	Arg	Ser	
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		595					600					605				
Leu	Gly	Tyr	Ser	Tyr	Ser	Arg	Asp	Leu	Asp	Leu	Ala	Lys	Lys	Lys	His	
	610					615					620					
Ala	Ser	Leu	Arg	Gln	Thr	Glu	Ser	Asp	Pro	Asp	Ala	Asp	Arg	Thr	Thr	
625					630					635					640	
Leu	Asn	His	Ala	Asp	His	Ser	Ser	Lys	Ile	Val	Gln	His	Arg	Leu	Leu	
				645					650					655		
Ser	Arg	Gln	Glu	Glu	Leu	Lys	Glu	Arg	Ala	Arg	Val	Leu	Leu	Glu	Gln	
			660					665					670			
Ala	Arg	Arg	Asp	Ala	Ala	Leu	Lys	Ala	Gly	Asn	Lys	His	Asn	Thr	Asn	

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Glu	Arg	Arg	Arg	Gln	Leu	Arg	Glu	Arg	Ala	Arg	Gln	Leu	Ile	Ala	Glu
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Ala	Arg	Ser	Gly	Val	Lys	Met	Ser	Glu	Leu	Pro	Ser	Tyr	Gly	Glu	Met
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Ala	Ala	Glu	Lys	Leu	Lys	Glu	Arg	Ser	Lys	Ala	Ser	Gly	Asp	Glu	Asn
			740					745					750		
Asp	Asn	Ile	Glu	Ile	Asp	Thr	Asn	Glu	Glu	Ile	Pro	Glu	Gly	Phe	Val
		755					760					765			
Val	Gly	Gly	Gly	Asp	Glu	Leu	Thr	Asn	Leu	Glu	Asn	Asp	Leu	Asp	Thr
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Pro	Glu	Gln	Asn	Ser	Lys	Leu	Val	Asp	Leu	Lys	Leu	Lys	Lys	Leu	Leu
785					790					795					800
Glu	Val	Gln	Pro	Gln	Val	Ala	Asn	Ser	Pro	Ser	Ser	Ala	Ala	Gln	Lys
				805					810					815	
Ala	Val	Thr	Glu	Ser	Ser	Glu	Gln	Asp	Met	Lys	Ser	Gly	Thr	Glu	Asp
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Val	Val	Phe	Ser	Lys	Asp	Ser	Thr	Val	Arg	Lys	Thr	Gln	Leu	Gln	Ser
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Phe	Ser	Gln	Tyr	Ile	Glu	Asn	Arg	Pro	Glu	Met	Lys	Arg	Gln	Arg	Ser
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Ile	Gln	Glu	Asp	Thr	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Ala	Ala	Ile	Thr
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Lys	Asp	Thr	Ser	Gln	Tyr	Val	Val	Gly	Glu	Leu	Ala	Ala	Leu	Glu	Asn
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Arg	Tyr	Leu	Met	Asp	Thr	Gly	Arg	Asn	Thr	Glu	Glu	Glu	Glu	Ala	Met	945	950	955	960
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Asp	Trp	Gln	Lys	Thr	Glu	Ala	Gln	Lys	Arg	Arg	Glu	Gln	Leu	Leu	Leu	1010	1015	1020	
Asp	Glu	Leu	Val	Ala	Leu	Val	Asn	Lys	Arg	Asp	Ala	Leu	Val	Arg	Asp	1025	1030	1035	1040
Leu	Asp	Ala	Gln	Glu	Lys	Gln	Ala	Glu	Glu	Glu	Asp	Glu	His	Leu	Glu	1045	1050	1055	
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Cys	Val	Leu	Gln													1075			

1

26